What is claimed:

1. A method for increasing metabolic flux through the pentose phosphate pathway in a microorganism comprising culturing a microorganism comprising a gene which is deregulated under conditions such that metabolic flux through the pentose phosphate pathway is increased.

2. The method of claim 1, wherein fructose or sucrose is used as a carbon source.

3. The method of claim 1, wherein fructose is used as a carbon source.

4. The method of claim 1, wherein the gene is fructose-1,6-bisphosphatase.

5. The method of claim 4, wherein the fructose-1,6-bisphosphatase gene is derived from *Corynebacterium*.

6. The method of claim 4, wherein the fructose-1,6-bisphosphatase gene is overexpressed.

7. The method of claim 1, wherein the gene encodes fructose-1,6-bisphosphatase.

8. The method of claim 7, wherein fructose-1,6-bisphosphatase has increased activity.

9. The method of claim 1, wherein the microorganism is a Gram positive microorganism.

10. The method of claim 1, wherein the microorganism belongs to the genus *Corynebacterium*.

11. The method of claim 10, wherein the microorganism is *Corynebacterium glutamicum*.

12. The method of claim 1, wherein the microorganism is fermented to produce a fine chemical.

13. The method of claim 1, wherein the microorganism further comprises one or more additional deregulated gene.

14. The method of claim 13, wherein the one or more additional deregulated gene is selected from the group consisting of an ask gene, a dapA gene, an asd gene, a dapB gene, a ddh gene, a lysA gene, a lysE gene, a pycA gene, a zwf gene, a pepCL gene, a

gap gene, a zwa1 gene, a tkt gene, a tad gene, a mqo gene, a tpi gene, a pgk gene, and a sigC gene.

15. The method of claim 14, wherein the one or more additional deregulated gene is overexpressed.

16. The method of claim 13, wherein the one or more additional deregulated gene encodes a protein selected from the group consisting of a feed-back resistant aspartokinase, a dihydrodipicolinate synthase, an aspartate semialdehyde dehydrogenase, a dihydrodipicolinate reductase, a diaminopimelate dehydrogenase, a diaminopimelate epimerase, a lysine exporter, a pyruvate carboxylase, a glucose-6-phosphate dehydrogenase, a phosphoenolpyruvate carboxylase, a glyceraldedyde-3-phosphate dehydrogenase, an RPF protein precursor, a transketolase, a transaldolase, a menaquinine oxidoreductase, a triosephosphate isomerase, a 3-phosphoglycerate kinase, and an RNA-polymerase sigma factor sigC.

17. The method of claim 16, wherein the protein has increased activity.

18. The method of claim 13, wherein the one or more additional deregulated gene is selected from the group consisting of a pepCK gene, a mal E gene, a glgA gene, a pgi gene, a dead gene, a menE gene, a citE gene, a mikE17 gene, a poxB gene, a zwa2 gene, and a sucC gene.

19. The method of claim 18, wherein the one or more additional deregulated gene is attenuated, decreased or repressed.

20. The method of claim 13, wherein the one or more additional deregulated gene encodes a protein selected from the group consisting of a phosphoenolpyruvate carboxykinase, a malic enzyme, a glycogen synthase, a glucose-6-phosphate isomerase, an ATP dependent RNA helicase, an o-succinylbenzoic acid-CoA ligase, a citrate lyase beta chain, a transcriptional regulator, a pyruvate dehydrogenase, an RPF protein precursor, and a Succinyl-CoA-Synthetase.

21. The method of claim 20, wherein the protein has decreased activity.

22. A method for producing a fine chemical comprising:

a) culturing a microorganism in which fructose-1,6-bisphosphatase is deregulated; and

b) accumulating the fine chemical in the medium or in the cells of the microorganisms, thereby producing a fine chemical.

23. A method for producing a fine chemical comprising culturing a microorganism in which at least one pentose phosphosphate biosynthetic pathway gene or enzyme is deregulated under conditions such that the fine chemical is produced.

24. The method of claim 23, wherein said biosynthetic pathway gene is fructose-1,6-bisphosphatase.

25. The method of claim 23, wherein said biosynthetic pathway enzyme is fructose-1,6-bisphosphatase.

26. The method of claim 22 or 24, wherein fructose-1,6-bisphosphatase expression is increased.

27. The method of claim 22 or 25, wherein fructose-1,6-bisphosphatase activity is increased.

28. The method of claim 22 or 23, further comprising recovering the fine chemical.

29. The method of claim 22 or 23, wherein one or more additional gene is deregulated.

30. The method of claim 29, wherein the one or more additional deregulated gene is selected from the group consisting of an ask gene, a dapA gene, an asd gene, a dapB gene, a ddh gene, a lysA gene, a lysE gene, a pycA gene, a zwf gene, a pepCL gene, a gap gene, a zwa1 gene, a tkt gene, a tad gene, a mqo gene, a tpi gene, a pgk gene, and a sigC gene.

31. The method of claim 30, wherein the one or more additional deregulated gene is overexpressed.

32. The method of claim 29, wherein the one or more additional deregulated gene encodes a protein selected from the group consisting of a feed-back resistant aspartokinase, a dihydrodipicolinate synthase, an aspartate semialdehyde dehydrogenase, a dihydrodipicolinate reductase, a diaminopimelate dehydrogenase, a diaminopimelate epimerase, a lysine exporter, a pyruvate carboxylase, a glucose-6-phosphate dehydrogenase, a phosphoenolpyruvate carboxylase, a glyceraldedyde-3-phosphate dehydrogenase, an RPF protein precursor, a transketolase, a transaldolase, a

menaquinine oxidoreductase, a triosephosphate isomerase, a 3-phosphoglycerate kinase, and an RNA-polymerase sigma factor sigC.

33. The method of claim 32, wherein the protein has increased activity.

34. The method of claim 29, wherein the one or more additional deregulated gene is selected from the group consisting of a pepCK gene, a mal E gene, a glgA gene, a pgi gene, a dead gene, a menE gene, a citE gene, a mikE17 gene, a poxB gene, a zwa2 gene, and a sucC gene.

35. The method of claim 34, wherein the one or more additional deregulated gene is attenuated, decreased or repressed.

36. The method of claim 29, wherein the one or more additional deregulated gene encodes a protein selected from the group consisting of a phosphoenolpyruvate carboxykinase, a malic enzyme, a glycogen synthase, a glucose-6-phosphate isomerase, an ATP dependent RNA helicase, an o-succinylbenzoic acid-CoA ligase, a citrate lyase beta chain, a transcriptional regulator, a pyruvate dehydrogenase, an RPF protein precursor, and a Succinyl-CoA-Synthetase.

37. The method of claim 36, wherein the protein has decreased activity.

38. The method of claim 22 or 23, wherein the microorganism is a Gram positive microorganism.

39. The method of claim 22 or 23, wherein the microorganism belongs to the genus *Corynebacterium*.

40. The method of claim 39, wherein the microorganism is *Corynebacterium glutamicum*.

41. The method of claim 22 or 23, wherein the fine chemical is lysine.

42. The method of claim 41, wherein lysine is produced at a yield of at least 100 g/L.

43. The method of claim 41, wherein lysine is produced at a yield of at least 150 g/L.

44. The method of claim 22 or 23, wherein fructose or sucrose is used as a carbon source.

45. The method of claim 22 or 23, wherein fructose is used as a carbon source.

46. The method of claim 22 or 24, wherein fructose-1,6-bisphosphatase comprises the nucleotide sequence of SEQ ID NO:1.

47. The method of claim 22 or 24, wherein fructose-1,6-bisphosphatase encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:2.

48. A recombinant microorganism which has a deregulated pentose phosphate biosynthesis pathway.

49. A recombinant microorganism comprising a deregulated pentose phosphate biosynthesis gene.

50. The recombinant microorganism of claim 49, wherein said deregulated gene is fructose-1,6-bisphosphatase.

51. The recombinant microorganism of claim 50, wherein fructose-1,6-bisphosphatase expression is increased.

52. The recombinant microorganism of claim 50, wherein said fructose-1,6-bisphosphatase gene encodes a fructose-1,6-bisphosphatase protein having increased activity.

53. The recombinant microorganism of claim 49, wherein the microorganism belongs to the genus *Corynebacterium*.

54. The recombinant microorganism of claim 53, wherein the microorganism is *Corynebacterium glutamicum*.

55. A polypeptide encoded by the nucleotide sequence of SEQ ID NO:1, wherein said polypeptide has fructose-1,6-bisphosphatase activity.